>IPI00083978.2 ACCESSION:IPI00083978 NID: Homo sapiens (Human).
            SIMILAR TO CD63 PROTEIN.   IPI_human
            Length = 220

 Score = 456 bits (1160), Expect = e-127
 Identities = 216/216 (100%), Positives = 216/216 (100%)

Query: 33   AWLLLDRNNFLTAFDENNHFIVPISQILIGMGSSTVLFCLLGYIGIHNEIRWLLIVYAV
             AWLLLDRNNFLTAFDENNHFIVPISQILIGMGSSTVLFCLLGYIGIHNEIRWLLIVYAV
Sbjct: 5   AWLLLDRNNFLTAFDENNHFIVPISQILIGMGSSTVLFCLLGYIGIHNEIRWLLIVYAV

Query: 93   ITWTFAVQVVLSAFIITKKEEVQQLWHDKIDFVISEYGSKDKPEDITKWTILNALQKTL
             ITWTFAVQVVLSAFIITKKEEVQQLWHDKIDFVISEYGSKDKPEDITKWTILNALQKTL
Sbjct: 65   ITWTFAVQVVLSAFIITKKEEVQQLWHDKIDFVISEYGSKDKPEDITKWTILNALQKTL

Query: 153   CCGQHNYTDWIKNKNKENSGQVPCSCTKSTLRKWFCDEPLNATYLEGCENKISAWYNVN
             CCGQHNYTDWIKNKNKENSGQVPCSCTKSTLRKWFCDEPLNATYLEGCENKISAWYNVN
Sbjct: 125   CCGQHNYTDWIKNKNKENSGQVPCSCTKSTLRKWFCDEPLNATYLEGCENKISAWYNVN

Query: 213   LTLIGINFGLLTSEVFQVSLTVCFFKNIKNIIHAEM 248
             LTLIGINFGLLTSEVFQVSLTVCFFKNIKNIIHAEM
Sbjct: 185   LTLIGINFGLLTSEVFQVSLTVCFFKNIKNIIHAEM 220

```
FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000
Please cite:
W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448


/tmp/fastaCAABDaabr: 248 aa
>LEX 121 Seq id no 2
vs  /tmp/fastaDAACDaabr library
searching /tmp/fastaDAACDaabr library


     220 residues in      1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
 join: 36, opt: 24, gap-pen: -12/ -2, width:  16
 Scan time:  0.000
The best scores are:                                        opt
gi|20553887|ref|XP_084868.4| similar to CD63 prot  ( 220) 1497

>>gi|20553887|ref|XP_084868.4| similar to CD63 protein [  (220 aa)
 initn: 1497 init1: 1497 opt: 1497
Smith-Waterman score: 1497;  100.000% identity in 220 aa overlap (29-248:1-220)


              10        20        30        40        50        60
LEX    MLRNNKTIIIKYFLNLINGAFLVLGLLFMGFGAWLLLDRNNFLTAFDENNHFIVPISQIL
                                  ::::::::::::::::::::::::::::::::
gi|205                           MGFGAWLLLDRNNFLTAFDENNHFIVPISQIL
                                         10        20        30


              70        80        90       100       110       120
LEX    IGMGSSTVLFCLLGYIGIHNEIRWLLIVYAVLITWTFAVQVVLSAFIITKKEEVQQLWHD
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|205 IGMGSSTVLFCLLGYIGIHNEIRWLLIVYAVLITWTFAVQVVLSAFIITKKEEVQQLWHD
           40        50        60        70        80        90


             130       140       150       160       170       180
LEX    KIDFVISEYGSKDKPEDITKWTILNALQKTLQCCGQHNYTDWIKNKNKENSGQVPCSCTK
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|205 KIDFVISEYGSKDKPEDITKWTILNALQKTLQCCGQHNYTDWIKNKNKENSGQVPCSCTK
          100       110       120       130       140       150


             190       200       210       220       230       240
LEX    STLRKWFCDEPLNATYLEGCENKISAWYNVNVLTLIGINFGLLTSEVFQVSLTVCFFKNI
       ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|205 STLRKWFCDEPLNATYLEGCENKISAWYNVNVLTLIGINFGLLTSEVFQVSLTVCFFKNI
          160       170       180       190       200       210


LEX    KNIIHAEM
       ::::::::
gi|205 KNIIHAEM
          220


 248 residues in 1 query    sequences
 220 residues in 1 library sequences
  Scomplib [version 3.3t05 March 30, 2000]
  start: Thu Aug 28 14:24:02 2003 done: Thu Aug 28 14:24:02 2003
  Scan time:  0.000 Display time:  0.067
```

Function used was FASTA